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Title:
Perfect score:
Sequence:

US-09-551-336B-1 45

1 AAAAAAAAAAK 11

February 19, 2004, 10:01:13 ; Search time 41 Seconds (without alignments) 42.585 Million cell updates/sec

OM protein - protein search, using sw model

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

Run on:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

1107863 seqs, 158726573 residues

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Maximum Match 100%
Listing first 45 so
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                                                                                                                                                                                                                                                                                       SUMMARIES
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	Li	Listing first 45 summaries
	» I	Geneseq_19Jun03:*
	۲.	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
	2:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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	4:	/gcgdata/geneseq/geneseqp-embl
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	6:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
	7:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
	æ :-	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
	9:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
	10:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
	11:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
	12:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
	13:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
	14:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
	15:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
	16:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
	17:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*
	18:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
	19:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
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Z	1.5	the number of results predicted by chance to have a
o O	reater	greater than or equal to the score of the result being printed,
Ď,	derive	is derived by analysis of the total score distribution

sult No.	Score	Query Match Length	ength)	8	ID "	<	Description	
9	45	100.0	16	18	AAW32224	1	Beta-sheet forming	
Ò	45	100.0	16	18	AAW32226		Beta-sheet forming	
(3)	45	100.0	17	18	AAW32227		Beta-sheet forming	_
4	45	100.0	20	24	ABP59409		Self-assembling di	_
5	45	100.0	30	24	ABP59422		Self-assembling tr	
6	45	100.0	30	24	ABP59423		Self-assembling tr	_
7	45	100.0	97	22	AAG75920		Human colon cancer	
00	45	100.0	201	23	ABP41465		Human ovarian anti	
9	45	100.0	216	23	ABP62982		Human polypeptide	_

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(TORR-) TORREY PINES INST MOLECULAR STUDIES.

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45	44	43	42	41	40	39	38	37	36	35	34	111	32	31	30	29	28	27	\ 26	25	24	23	22	21	20	19	18	/ 17	716	15	14	13	12	11	/ 10
42	42	42	42	42	42	42	42	42	42	42	42	5	45	45	45	45	4 5	45	4 5	4 5	45	4 5	45	4 5	5	4 5	45	45	45	4 .	45	45	45	45	45
93.3	93.3		93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		100.0	•	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
244	229	161	157	157	102	102	102	31	30	30	20	733	733	731	731	730	730	730	712	869	869	660	571	515	406	335	265	262	226	225	221	220	220	218	218
22	23	21	24	22	24	24	24	21	24	24	24	20	15	22	21	23	21	19	21	21	20	20	21	21	22	22	21	22	17	21	23	24	23	21	21
ABG21054	ABP41248	AAB19319	ABU55441	AAU16372	ABJ20256	ABJ20253	ABJ20243	AAB08166	ABP59425	ABP59424	ABP59411	AAY01301	AAR56653	AAB66657	AAY69068	AA017360	AAB08631	AAW46315	AAB08630	AAY69069	AAY01302	AAY01303	AAY69071	AAY69135	AAB95251	ABB58955	AAB58221	ABG15586	AAW05151	AAG00758	ABP62855	ABU07443	AAU76972	AAG00759	AAG00755
Novel human diagno	Human ovarian anti	Amino acid sequenc	Human novel polype	sec	162P1E6 cancer gen	162P1E6 cancer gen		Peptide modulating	Self-assembling tr	Self-assembling tr	Self-assembling di	Amino acid sequenc	Synthetic human tr	Human elastin prot	Amino acid sequenc	Human elastin. Ho	Fusion protein com	Human elastin cont /	Amino acid sequenc	Amino acid sequenc	Human tropoelastin ,	Human tropoelastin	Amino acid sequenc	Amino acid sequenc	Human protein sequ	Drosophila melanog	Lung cancer associ	Novel human diagno	Nuclear proliferat	Human secreted pro	Human polypeptide	Protein differenti	$\mathbf{-}$		Human secreted pro

ALIGNMENTS

PR	뭐	g	Ž.	g X	Ŧ	FT	Ϋ́	ΕŢ	FH	X	သ	X	W	₹	Š	×	ద	×	ij	×	AC	×	ij	AAW	RES
26-MAY-1995;	23-MAY-1996;	28-NOV-1996.		W096372121A1.		Modified-site		Modified-site	Key		Synthetic.		neurodegenerat	phosphodiestera	Beta sheet; ci:		Beta-sheet for		12-FEB-1998 (;		AAW32224;		AAW32224 standa	AAW32224	RESULT 1
95US-0452043.	96WO-US07564.	Juve Good			/note= "C-terminal amide"	16	/note= "N-terminal acetyl"		Location/Qualifiers				neurodegenerative disease; Alzheimer's disease; amyloid deposition.		Beta sheet; circular dichroism spectroscopy; glycosidase activity;	1	Beta-sheet forming peptide #1.		(first entry)				AAW32224 standard; peptide; 16 AA.		

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RESULT 2
AAW32226
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a specific example of a polypeptide, which forms a beta sheet in an aqueous environment and has the general formula JnAmiXuAm2Jn or Ac-JlnAmiXuAm2Jn-NH2, in which A = D- or L-alanine amino acid; ml m2 = 0.40; ml+m2 = 10.40; J = a charged amino acid; n = 1 or 2; X = any amino acid except proline; u = 0 or 1; Jl lysine, hydroxylysine, arginine, histidine, aspartic acid, glutamic acid or gamma-carboxyglutamic acid; Ac = an acylation modification to the amino terminus; NH2 = an amidation modification to the carboxylic acid terminus; and X1 = cysteine, threonine, tyrosine or serine. The peptides have phosphodiesterase activity and readily hydrolyse nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beta sheet; circular dichroism spectroscopy; glycosidase activity; phosphodiesterase activity; drug screening; hydrolysis; neurodegenerative disease; Alzheimer's disease; amyloid deposition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide(s) which form stable beta sheets in aq. environment having phosphodiesterase and glycosidase activity and useful in bio:engineering, enzymatic and drug screening applications
Blondelle SE,
                                                                                                                                                                                                                                                                                     W0963 (212-A1.
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                                                                                                                                26-MAY-1995;
                                                                                                                                                                                       23-MAY-1996;
                                                                                                                                                                                                                                            28-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beta-sheet forming peptide #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW32226 standard; peptide; 16
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                                                                        (TORR-) TORREY PINES INST MOLECULAR STUDIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
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              Forood B, Houghten RA,
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                                                                                                                                95US-0452043.
                                                                                                                                                                                       96WO-US07564.
                                                                                                                                                                                                                                                                                                                                                                                     /note= "N-terminal acetyl"
16
                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB 18;
Pred. No. 0.31;
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                    Perez-paya E;
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forms a beta sheet in an aqueous environment and has the general formula JUANHIXIAMAZIO OR AC-JUANHIXIAMAZIO-NH2, in which A = D- or I-alanine amino acid; m1, m2 = 0-40; m1+m2 = 10-40; J = a charged amino acid; n = 1 or 2; X = any amino acid except proline; u = 0 or 1; J1 lysine, hydroxylysine, arginine, histidine, aspartic acid, glutamic acid or hydroxylysine, arginine, histidine, aspartic acid, glutamic acid or gamma-carboxyglutamic acid; Ac = an acylation modification to the amino terminus; NH2 = an amidation modification to the carboxylic acid terminus; and X1 = cysteine, threonine, tyrosine or serine. The peptides have phosphodiesterase activity and readily hydrolyse nucleic acids.
                                                   They also have glycosidase activity and readily hydrolyse sugar phosphates. Further they can cause amine-catalysed decarboxylation (e.g. decarboxylation of oxalacetate), and they can hydrolyse phospholipids. They can be used for bioengineering, enzymatic and drug screening applications. In particular they can be used for screening drugs for the prevention or treatment of neurodegenerative diseases, e.g. Alzheimer's disease, which result in amyloid protein deposition. They can also be used to screen for drugs which inhibit or disrupt the beta sheet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 15; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     having phosphodiesterase and glycosidase activity and usef-
bio:engineering, enzymatic and drug screening applications
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptide(s) which form stable beta sheets in aq. environment
having phosphodiesterase and glycosidase activity and useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-033944/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a specific example of a
   16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fic example of a polypeptide, which environment and has the general for
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9

Matches Query Match Best Local S σ 1 AAAAAAAAAK 11 Similarity Conservative 100 . 0 0 Score 45; DB 1 Pred. No. 0.31; Mismatches DB 18; 0 Length 16; Indels 0; Gaps

0

RESULT 3
AAW32227
ID AAW3
XX AAW32227
AC AAW3
XX Beta
XX Beta
XX Beta
XX Beta
XX Beta
XX Phos

XX W neur
XX Key
FT Modi
FT Mod Beta-sheet 12-FEB-1998 AAW32227; AAW32227 standard; peptide; forming peptide #3. (first 17

Beta sheet; circular dichroism spectroscopy; glycosidase activity; phosphodiesterase activity; drug screening; hydrolysis; neurodegenerative disease; Alzheimer's disease; amyloid deposition

Synthetic

28-NOV-1996. W096372127-A1 Modified-site 23-MAY-1996; Modified-site 96WO-US07564 /note= "N-terminal acetyl"
17 /note= "C-terminal amide" Location/Qualifiers

26-MAY-1995; (TORR-) TORREY PINES INST MOLECULAR STUDIES 95US-0452043.

Blondelle SE, Forood B, Houghten RA, Perez-paya

Example 2; Page 16; 35pp; English

Polypeptide(s) which form stable beta sheets in aq. environment having phosphodiesterase and glycosidase activity and useful in bio:engineering, enzymatic and drug screening applications

WPI; 1997-033944/03

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RESULT 4
ABP59409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a specific example of a polypeptide, which CC forms a beta sheet in an aqueous environment and has the general formula CI JNAmIXLAMAZJON or Ac-JINAMIXLLAMAZJON-NH2, in which A = D or L-alanine CC amino acid; ml, m2 = 0-40; ml+m2 = 10-40; J = a charged amino acid; n = 1 CC or 2; X = any amino acid except proline; u = 0 or 1; Jl lysine, CC hydroxylysine, arginine, histidine, aspartic acid, glutamic acid or CC gamma-carboxyglutamic acid; Ac = an acylation modification to the amino CC terminus; NH2 = an amidation modification to the carboxylic acid CC terminus; and X1 = cysteine, threenine, tyrosine or serine. The peptides CC have phosphodissterase activity and readily hydrolyse nucleic acids. CC They also have glycosidase activity and readily hydrolyse sugar CC phosphates. Further they can cause amine-catalysed decarboxylation (e.g. CC decarboxylation of oxalacetate), and they can hydrolyse phospholipids. CC They can be used for bioengineering, enzymatic and drug screening CC applications. In particular they can be used for screening drugs for the prevention or treatment of neurodegenerative diseases, e.g. Alzheimer's CC disease, which result in amyloid protein deposition. They can also be comply the period of the carboxylation for drugs which inhibit or disrupt the beta sheet.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                    Self-assembling di-block oligopeptide AK20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP59409 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                 Self-assembling oligopeptide; dipolar; nanotube; nanostructure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP59409
                                                                                                                                                                                                                                                     10-JUL-2002; 2002WO-US21757
                                                                                                                                                                                                                                                                                      23-JAN-2003.
                                                                                                                                                                                                                                                                                                                   WO2003006043-A1
The present invention relates to/self-assembling dipolar oligopeptides
                                                                                                                                                 Zhang S,
                               Claim 16; Page 21)
                                                                   drug delivery
                                                                                  New dipolar oligopeptides in a self-assembled nanostructure useful for
                                                                                                                   WPI; 2003-267944/26.
                                                                                                                                                                                   (MASI ) MASSACHUSETTS INST TECHNOLOGY
                                                                                                                                                                                                               10-JUL-2001; 2001US-304256P
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                                                                                                                                                  Vauthey S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17
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A
                                                                                                                                                                                                                                                                                                                                                                                       carrier
                               52pp; English
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Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 17;
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and di-and tri-block peptide copolymers. The dipolar oligopeptides have ability to self assemble to form stable nanotubes. The self-assembled nanostructure have the ability to entrap and deliver molecules with high degree of efficacy. The copolymers are amenable for molecular systematic design, modification and synthesis; can be subjected to extensive molecular modelling and simulations before synthesis; can be highly purified to be mono-dispersed materials; combinatorial approach can be employed to systematically characterize these co-polymers at various ratio; and can be synthesized in vitro or in vivo. The nanotubes fuse with the lipid bilayers and do not deform the cells as liposomes do. The oligopeptides can be used in a self-assembled nanostructue (e.g. nanotube) for delivering drug into a cell and as a carrier for

The present invention relates to self-assembling dipolar oligopeptides

New dipolar oligopeptides in a self-assembled nanostructure useful for

grug

Zhang S,

Vauthey S;

(MASI) MASSACHUSETTS INST TECHNOLOGY

Claim 21; Page 23; 52pp; English

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RESULT 5
ABP59422
ID ABP5
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Self-assembling tri-block oligopeptide KAK30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP59422;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              purified to be mono-dispersed materials; combinatorial approach can be employed to systematically characterize these co-polymers at various ratio; and can be synthesized in vitro or in vivo. The nanotubes fuse with the lipid bilayers and do not deform the cells as liposomes do.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       molecular modelling and simulations before synthesis; can be highly
                                                                                                                                                                                                                                                                                                                             10-JUL-2001; 2001US-304256P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Self-assembling oligopeptide; dipolar; nanotube; nanostructure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               di-block oligopeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            drug delivery; carrier.
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biologically active materials. tri-block oligopeptide.

The present sequence is one such

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                                                                                                                                                                       degree of efficacy. The copolymers are amenable for molecular systematic design, modification and synthesis; can be subjected to extensive molecular modelling and simulations before synthesis; can be highly purified to be mono-dispersed materials; combinatorial approach can be employed to systematically characterize these co-polymers at various ratio; and can be synthesized in vitro or in vivo. The nanotubes fuse with the lipid bilayers and do not deform the cells as liposomes do.
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                                                                                                                                                                                                                                                             The present invention relates to self-assembling dipolar oligopeptides and di-and tri-block peptide copolymers. The dipolar oligopeptides have ability to self assemble to form stable nanotubes. The self-assembled nanostructure have the ability to entrap and deliver molecules with high
                                                                                                                                                                                                                                                                                                                            Claim 23; Page 23; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                               New dipolar oligopeptides in a self-assembled nanostructure useful
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-267944/26.
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RESULT 8
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ABP41465 standard; Protein;

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RESULT 7
AAG75920
ID AAG75920
ID AAG75920
AC AAG77
XX AAG78
AC AAG77
XX AAG77
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                                                                                                                                                                                                                                                                                                                                                             CC ancer-associated nucleic acid molecules (N) and proteins (P), where colon cancer antigens have cytostatic acitivity and can be used in gene colon cancer antigens have cytostatic activity and can be used in gene colon cancer antigens have cytostatic activity and can be used in gene colon cancer antigens have cytostatic activity and can be used in the prevention, colors and treatment of diseases associated with inappropriate P cc expression. For example, N and P may be used to treat disorders color associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing cc inactive proteins or to supplement the patients own production of P. canditionally, N may be used to produce the colon cancer-associated Ps, inserting the nucleic acids into a host cell and culturing the cell color inserting the proteins. N and P can be used in the prevention, diagnosis colorestal carcinomas and cancers. AAH37196 to AAH37204 and AAB7789 represent sequences used in the exemplification of the
                                                                  Matches
                                                                                            Query Match
Best Local (
                                                                                                                                                                                                                                              \bar{N}.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
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03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
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                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                             present invention.
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                                                                  Conservative
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Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ovarian antigen HOOJO38, SEQ ID NO:2597
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Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases

Birse CE,

Rosen CA

ABQ54542.

07-JUN-2000; 2000US-209467P 07-JUN-2001; 2001WO-US18569

(HUMA-) HUMAN GENOME SCI INC

Claim 11; SEQ ID No 2597; 2922pp; English

blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disor and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The pres sequence represents a human ovarian antigen of the invention.

Note: The sequence data for this patent did not form part of the prin specification, but was obtained in electronic format directly from WI disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), block-related disorders, autoimmune oophoritis, systemic lupus erythematosus), encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related treating, prognosing or preventing various ovary and/or breast-related The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to CDNAs encoding them (ABQ54131-ABQ56305), and also ftp.wipo.int/pub/published_pct_sequences. of form part of the printed format directly from WIPO disorders present may

Sequence 201

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Matches

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Conservative

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Best Local Similarity
                                                                                                                                                                                                  The invention relates to an isolated polynucleotide (I) comprising one 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising administering to a mammalian subject a composition comprising the prote (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II). (II) and (III) are useful for diagnostic evaluation of disorders. (I) is useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound heali and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's, Parkinson's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies
                                                                               Sequence
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N-PSDB; ABQ93461.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP62982 standard; Protein; 216 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 419; 284pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-SEP-2000; 2000US-0654935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune disorder; multiple sclerosis; diabetes; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiparkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP62982
                                                                                                                                                         specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkinson's disease; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antidiabetic;
                                                                                                                        re: The sequence data for this patent did not acification, but was obtained in electronic for ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E, Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asundi V,
Wang D, 1
                                                                               216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ary; dermatological; neuroprotective; nootropic; cancer; ian; immunostimulant; cytostatic; immunosuppressive; antiallergic; gene therapy; wound healing; tissue repai nervous system disorder; Alzhimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /, Zhou
Liu C,
  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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Drmanac RT,
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Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ren F, ;
Wehrman
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                           DB
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n T;
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                                                                                                                                                         part of the printed directly from WIPO
                              216;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                              g the protein to (II).
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RESULT 10
AAG00755
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AAG00759
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                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedur
                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; SEQ ID 4836; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dumas Milne Edwards J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy;
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             06-OCT-2000
                                        AAG00759;
                                                                  AAG00759
                                                                                                                                                                                                                                                                                  regulatory sequences and to design expression and secretion vectors
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DB; AAC00761.
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                                                                                                                                                                                                              Similarity
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                                                                                                                                                                    AAAAAAAAAK 11
                                                                  standard;
                                                                                                                                        AAAAAAAAAAK 165
                                                                                                                                                                                                                                                       218 AA;
                                                                                                                                                                                                Conservative
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           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome mapping.
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                                                                    Protein;
                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy and chromosome mapping procedures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218
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                                                                                                                                                                                            Score 45; DB 21; Pred. No. 3.6; Mismatches 0;
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RESULT 12
AAU76972
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Best Local S
Matches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 200
N-PSDB;
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                                                                      carcinoma; non-small cell carcinoma; smoking; lung cancer; bladder cancer; head cancer; neck cancer; urothelial cancer; kidney cancer; pancreas cancer; mouth cancer; throat cancer; pharynx cancer; larynx cancer; upper airway primary cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; SEQ ID 4840; 71pp + CD-ROM; English
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                                                                                                                                                                                                                                                                                                                                                                                                            AAU76972 standard;
Homo sapiens
                                                upper airway secondary cancer;
                                                                                                                                                                                     Ribosomal L14 protein; RPL14; CD39L3; PMGM; GC20; cancer; metastasis;
                                                                                                                                                                                                                                             Human ribosomal L14 (RPL14) protein.
                                                                                                                                                                                                                                                                                                   21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                         AAU76972;
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                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                               220
                                                     esophagus cancer; chromosome 3p21.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Giordano
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 development of cancer, predicting progression or metastasis of non-small cell carcinoma and other carcinoma in a subject, or identifying an individual to be segregated from a high risk environment. The method comprises contacting an RPL14, CD39L3, PMGM, or GC20 gene probe with a test sample obtained from a subject, and analysing DNA from the test sample. The method is useful for identifying a subject (a smoker, non-smoker or former smoker) at risk for the development, recurrence, or metastasis of cancer (preferably cancer of lung, bladder, head, neck, urothelial, kidney, pancreas, mouth, throat, pharynx, larynx or seophagus, or an upper airway primary or secondary cancer), to identify subjects who need an intensive follow-up protocol and for the prognosis and diagnosis of cancer. This is the amino acid sequence of the human ribosomal L14 protein (RPL14, located on chromosome 3921.3), used to develop the gene probe described in the method of the invention.
                                                                                                                                                                                             Prostate cancer; gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 69-70; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying subject at risk for development of cancer, preferably lung cancer, comprises contacting RPL14, CD39L3, PMGM, or GC20 gene probe with test sample obtained from subject, and analysing DNA from test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                           28-JAN-2003
                                                                                                                                                                                                                                                                                                        ABU07443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a method of identifying a subject at
                                                                                                                     WO200281638-A2
                                                                                                                                                                                                                                           Protein differentially regulated in prostate cancer #46.
                                                                                                                                                                                                                                                                                                                                      ABU07443 standard;
                                                          08-APR-2002; 2002WO-US10824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-217200/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AAAAAAAAAAA 11
                                                                                                                                                                             staging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK10349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jiang
                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAAAAAAK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ă,
                                                                                                                                                                               drug target; cancer detection; cancer diagnosis; ancer grading; cancer assessing; cancer monitorin
                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45; DB Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 220;
                                                                                                                                                                                cancer monitoring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      risk for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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06-APR-2001; 2001US-281731P 06-APR-2001; 2001US-281732P

RESULT 14
ABP62855
ID ABP62
XX ABP62
XX ABP62
XX ABP62
XX 14-OC
DT 14-OC
XX Human
XX Human
XX Human
XX Human
XW Antig
KW Antig
KW Antig

(first entry)

Human 14-OCT-2002 ABP62855

polypeptide

SEQ ID NO 292.

ABP62855 standard; Protein; 221 AA

Human; vulnerary; dermatological; neuroprotective; nootropic; cancer; antiparkinsonian; immunostimulant; cytostatic; immunosuppressive; antidiabetic; antiallergic; gene therapy; wound healing; tissue repai. burn; central nervous system disorder; Alzheimer's disease;

repair

밁 Ś

Matches

11; μ

Conservative

0

AAAAAAAAAK 11

Query Match Best Local Similarity

100.0%;

Score 45; DB Pred. No. 3.6; Mismatches

24; 0,

Length 220;

0

Gaps

0;

Sequence

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cc diagnosing, staging, grading, assessing, monitoring, prognosticating, cc preventing or treating, determining prediagosition to diseases and conditions especially relating to prostate cancer. (I) and its expression conditions especially relating to prostate cancer. (I) and its expression cc products are used in the diagnostic test to assay for presence of cancer ce.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in blood etc. (I) is useful for assessing cancer e.g., to determine the type of cancer, its stage of development, the nature of genetic defect, etc. crapped to the polypeptide encoded by (I) can be used as target for therapy or drug concevery. (I) can also be used for expressing the polypeptide and thus cross-till in therapeutic applications to treat prostate cancer. The constitution of specific genes, and groups of genes, expressed in confict the pathways physiologically relevant to prostate cancer permits the confiction of functional and disease pathways and the delineation of targets in these pathways which are useful in diagnostic, therapeutic, and clinical applications. This is the amino acid sequence of a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preferably, the expression levels of at least 10 genes are determined. (I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells, which involves contacting a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, and the contact of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intervention in a subject having a prostate cancer, which involves determining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of target genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sample comprising prostate tissue, which involves determining the number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes genes (I) which are differentially regulated prostate cancer (I) Is useful for diagnosing a prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ORIG-) ORIGENE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is indicative of the probability that the sample comprises ancer. (I) Is useful for assessing a therapeutic or preventive
220 AA;
                                                                               regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297; 416pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     which are differentially-regulated
                                                                               in prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in the sample,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             where
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RESULT 15
AAG00758
ID AAG00
XX AAG00
XX AAG00
XX D6-OC
XX Human
XX Human
XX Human
XX Human
XX Homo
XX Homo
XX Homo
XX Homo
XX EP10:
XX PD 06-S]
                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated polynucleotide (I) comprising one of 245 sequences (AB093288-AB093532). Treating a condition comprising administering to a mammalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II). (II) and (III) are useful for diagnostic evaluation of disorders. (I) is useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's, Parkinson's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parkinson's disease; Huntington's disease; immune disorder; autoimmune disorder; multiple sclerosis; diabetes; allergy.
                06-SEP-2000
                                             EP1033401-A2
                                                                       Homo sapiens
                                                                                                   gene therapy;
                                                                                                                    Human;
                                                                                                                                               Human secreted protein, SEQ ID NO: 4839.
                                                                                                                                                                             06-OCT-2000
                                                                                                                                                                                                                                    AAG00758 standard; Protein; 225
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 292; 284pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABQ93334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-583321/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-SEP-2000; 2000US-0654935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-AUG-2001; 2001WO-US27093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200218424-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QA,
                                                                                                                                                                                                                                                                                                              156
                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                         سر
                                                                                                                  5' EST;
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                              AAAAAAAAAK 166
                                                                                                                                                                                                                                                                                                                                       AAAAAAAAAK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asundi V, zı.
                                                                                                                                                                                                                                                                                                                                                                                                                               221 AA;
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                             (first entry)
                                                                                                   chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhou P,
iu C, Dr
                                                                                                                 sequence tag; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P, Xue AJ,
Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wehrman
                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Η,
                                                                                                                                                                                                                                                                                                                                                                                                 Length 221;
                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ġ,
                                                                                                                    cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang J;
                                                                                                                                                                                                                                                                                                                                                                      ۰,
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                               S
                                                                                    Query Match
Best Local 9
                                                                       Matches
                                                                                                                                                                                         The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic onds and can therefore be used to obtain full length cDNAs and genomic cohromosome mapping procedures. They are used to obtain upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-500381/45.
N-PSDB; AAC00764.
                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; SEQ ID 4839; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-FEB-2000; 2000EP-0200610
                                                                                                                                                                             regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEST ) GENSET
162 AAAAAAAAAK 172
                                                                     11;
                                   1 AAAAAAAAAAK 11
                                                                                     Similarity
                                                                                                                                          225 AA;
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0122487
                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duclert A,
                                                                       0
                                                                     Score 45; DB
Pred. No. 3.7
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Giordano
                                                                                  DB . 7;
                                                                                                        21;
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                                                                       <u>.</u>
                                                                                                    Length 225;
                                                                       Indels
                                                                       0;
                                                                       Gaps
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Search completed: February 19, 2004, 10:03:18 Job time : 42 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               801455 seqs, 209382283 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

14		13	12	- 11	10	9		7		5	4	ω	2	/ 1	Result No.
4.5	45	45	45	45	45	45	45	45	45	45	45	45	45	45	Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match Length
104	104	104	104	104	104	104	104	104	97	79	79	30	30	20	ength
12	12	12	12	12	12	12	12	12	15	12	12	12	12	12	BB
US-10-177-725-42	US-10-177-725-38	US-10-177-725-37	US-10-177-725-36	US-10-177-725-35	US-10-177-725-34	US-10-177-725-33	US-10-177-725-32	US-10-177-725-31	US-10-106-698-6694	US-10-177-725-72	US-10-177-725-22	US-10-192-832-69	US-10-192-832-68	US-10-192-832-55	ID
Sequence 42,	Sequence 38,	Sequence 37,	Sequence 36,	Sequence 35,	Sequence 34,	Sequence 33,	Sequence 32,	Sequence 31,	Sequence 6694,	Sequence 72,	Sequence 22,	Sequence 69,	Sequence 68,	Sequence 55,	Description
App1	App1	App1	Appl	Appl	App1	App1	Appl	Appl	4, Ap	Appl	Appl	App1	Appl	Appl	!

RESULT 2
US-10-192-832-68
(S-equence 68, Application US/10192832
Publication No. US20030176335A1
GENERAL INFORMATION:

ALIGNMENTS

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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide US-10-192-832-55
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US-10-192-832-55
                                                                                                                                                                                                                                                                                                                           Sequence 55, Application US/10192832

Publication No. US20030176335A1

GENERAL INFORMATION:
APPLICANT: EMANG, SHUGUANG
APPLICANT: VAUTHEY, SYLVAIN

TITLE OF INVENTION: SURFACTIANT PEPTIDE NANOSTRUCTURES, AND USES THEREOF
FILE REFERENCE MTV-043.01

CURRENT APPLICATION NUMBER: US/10/192,832

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION UNMBER: 60/304,256
PRIOR PILING DATE: 2001-07-10

NUMBER OF SEQ ID NOS: 76

NUMBER OF SEQ ID NOS: 76
                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 55
LENGTH: 20
TYPE: PRT
                                                                     Query Match
Best Local Similarity 100
Matches 11; Conservative
                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                            1 AAAAAAAAAAK 11
                                                                                              100.0%; Score 45; DB 12; 100.0%; Pred. No. 0.32;
                                                                           0;
                                                                             Mismatches
                                                                           0;
                                                                                                                Length 20;
                                                                             Indels
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                                                                           Gaps
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US-10-177-725-22
; Sequence 22, Application US/10177725
; Publication No. US20030143562A1
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SEQ ID NO 68
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Publication No. US20030176335A1
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Best Local Similarity
Matches 11; Conserv
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LENGTH: 30
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                                                                                                                             GENERAL INFORMATION:
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TITLE OF INVENTION: SURFACTANT PEPTIDE NANOSTRUCTURES, AND USES THEREOF
FILE REFERENCE: MTV-043.01
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TITLE OF INVENTION: SURFACTANT PEPTIDE NANOSTRUCTURES, AND USES THEREOF
FILE REFERENCE: MTV-043.01
FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
                                                    APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT
                                                                       APPLICANT: Anderson, David
APPLICANT: Bogenberger, J
APPLICANT: Peele, Beau R.
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PRIOR FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 76
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CURRENT FILING DATE: 2002-07-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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1 Similarity 100.0%;
11; Conservative (
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                                                                                        Jakob M.
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Pred. No.
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US-10-106-698-6694

Sequence 6694, Application US/10106698 Publication No. US20030109690A1 GENERAL INFORMATION:

APPLICANT: Ruben et al.
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27

and Polypeptide

RESULT 6

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                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1
SEQ ID NO 72
LENGTH: 79
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                                                                               Best
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CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Anderson, David APPLICANT: Bogenberger, Ja APPLICANT: Peele, Beau R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 173
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                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 173
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TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
                                                                                                                                            LOCATION: (21). (52)
OTHER INFORMATION: "Xaa" at positions 21-23,
OTHER INFORMATION: 5, 47-48 and 50-52 can be
                                                                                                                                                                             NAME/KEY: MISC_FEATURE
LOCATION: (21)..(52)
                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                              OTHER INFORMATION: synthetic
                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                               ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT
                                                                               Local
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62 AAAAAAAAAAK 72
                             1 AAAAAAAAAAAK 11
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                                                                               Similarity
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                                                                Conservative
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                                                                               100.0%;
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                                                                               Score 45;
Pred. No.
                                                                  Mismatches
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PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28

APPLICATION NUMBER: US FILING DATE: 1999-09-29

60/157,137

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SEQ ID NO 31
LENGTH: 104
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LENGTH: 97
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Publication No. US20030143562A1
                                                                                                                                                                                   GENERAL INFORMATION:
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Best Local Similarity
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Best Local S
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APPLICANT: Bogenberger, Ja
APPLICANT: Peele, Beau R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
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                                                  FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT FILE REFERENCE: A-66900-4/RMS/AMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Anderson, David APPLICANT: Bogenberger, J
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                 PRIOR APPLICATION NUMBER: US 09/415,765 PRIOR FILING DATE: 1999-10-08
                                                                                                             TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial sequence
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ORGANISM: Homo sapiens
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RIOR APPLICATION NUMBER: US 09/169,015
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                                                                                                                                                                                                                                                                                                                     AAAAAAAAAK 103
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Peele, Beau R.
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Pred. No. 1.5;
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US-10-177-725-33
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                                                                                                                                                                                                                                                    Sequence 34, Application US/10177725
Publication No. US20030143562A1
GENERAL INFORMATION:
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SEQ ID NO 33
LENGTH: 104
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APPLICANT: Anderson, David
APPLICANT: Bogenberger, Ja
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Best Local Similarity 100.0%;
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APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Bedgenberger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILLING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR PELICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 173
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CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
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NUMBER OF SEQ ID NOS: 173
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TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT S
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TYPE: PRT
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Local Similarity 100.0%;
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Pred. No. 1.5;
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Pred. No. 1.5;
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RESULT 12
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SEQ ID NO 35
LENGTH: 104
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LENGTH: 104
TYPE: PRT
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Best Local Similarity
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SEQ ID NO 36
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                                                                                                                                                                                                                                FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
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CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF TIME DATE: 1998-10-08
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APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT FILE REFERENCE: A-66900-4/RMS/AMS
                                                                                                                    PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
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APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT FILE REFERENCE: A-66900-4/RMS/AMS
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APPLICANT: Bogenberger, Ja
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Pred. No. 1.5;
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SOFTWARE: Pa
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CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
                                              PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR TILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
                                                                                                                  CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
                                                                                                                                                                                  APPLICANT: Anderson, David
APPLICANT: Bogenberger, J
APPLICANT: Peele, Beau R.
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APPLICANT:
                                                                                                                                                   TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES FILE REFERENCE: A-66900-4/RMS/AMS
                                  NUMBER OF SEQ ID NOS: 173
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11; Conserv
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Pred. No.
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Pred. No.
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ORGANISM: Artificial sequence FEATURE:

OTHER INFORMATION: synthetic

TYPE: PRT

ENGTH:

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RESULT 15
US-10-177-725-42
US-10-177-725-42; Sequence 42, Application US/10177725; Publication No. US20030143562A1; GENERAL INFORWATION:
Search completed: February 19, 2004, 10:10:03 Job time : 35 secs
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                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
FOTHER INFORMATION: synthetic
US-10-177-725-42
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APPLICANT: Bogenberger, Jakob M.
APPLICANT: Begenberger, Jakob M.
APPLICANT: Peele, Beau R.

ITILE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT :

FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US/1177,725

CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR PILING DATE: 1999-10-08
PRIOR PILING DATE: 1998-10-08
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOUTWARE: Patentin version 3.1

SEQ ID NO 42
LENGTH: 104
                                                                                                                                                                                               Query Match 100.0%; Score 45; DB 12; Length 104; Best Local Similarity 100.0%; Pred. No. 1.5; Matches 11; Conservative 0; Mismatches 0; Indels (
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Result
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Maximum Match 10
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Maximum DB seq length: 200000000
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Perfect score:
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  Issued_Patents_AA:*
1: /cgn2_6/ptodata/1
2: /cgn2_6/ptodata/1
3: /cgn2_6/ptodata/1
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US-09-117-121-30
US-09-234-33-2-10
US-09-736-457-1813
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US-08-788-822A-15
US-08-788-92-288-6
US-07-999-784-6
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                                                                                                         TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-911-364-1
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RESULT 1
US-08-911-364-1
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RELEAR-NOT 5969106

GENERAL INFORMATION:
APPLICANT: ROTHSTEIN, Aser
APPLICANT: KEELY, Fred W.
APPLICANT: ROTHSTEIN, Steven J.
APPLICANT: ROTHSTEIN, STEVEN
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,364
FILING DATE: 07-AUG-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/023,552
FILING DATE: 07-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 041082/0104
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
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CITY: Washington
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Matches

Query Match Best Local Similarity

Conservative

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Mismatches

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Gaps

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100.0%;

Score 45; DB Pred. No. 1.8;

2;

Length 731; Indels

TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 731 amino acids

TELEPHONE:

(202) 672-5300

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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atent-No / 02221-10N:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: (MEISS,) ANTHONY S
APPLICANT: MARTIN, STEPHEN L
APPLICANT: MARTIN: SYNTHETIC POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
-09-340-736E-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 041082/0110
CURRENT APPLICATION NUMBER: US/09/340,736E
CURRENT FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 08/911,364
PRIOR FILING DATE: 1997-08-07
PRIOR APPLICATION NUMBER: 60/023,552
PRIOR FILING DATE: 1996-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ROTHSTEIN, STEVEN
FITTLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN
FITTLE OF INVENTION: AND OTHER FIBROUS PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC-compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                             APPLICATION NUMBER: FILING DATE: 28-JUN-PRIOR APPLICATION DATA:
                                                                     APPLICATION NUMBER: AU PL6520
FILING DATE: 22-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL9661
                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                   APPLICATION NUMBER: US/08/464,700 FILING DATE: 7-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-736E-1
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                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                            DDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                      Spring House Corporate Cntr, PO Box 457
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16-DEC-1993
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100.0%; Pred. No. 1.8;
               PCT/AU93/00655
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The Local Similarity
The Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 40% Application US/08678039A Parent No. (5858662)
Matches
                             Query Match
                Best Local
                                                                                                                                                        TELEFAX: 202-783-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 232:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-624-1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 733 amino acid
                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                          TELEPHONE: 202-0-
TELEPHONE: 202-783-6031
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/678,039A FILING DATE: 10-JUL-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GH
                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 555 Thirteenth
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TOPOLOGY: linear
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                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                         LENGTH:
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              h 100.0%; Score 45; Similarity 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington
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C
                                                                                                                        792 amino acids
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 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosis of Williams Syndrome and Diagnosis of Williams Syndrome Cognitive Profile by Analysis of the Williams Syndrome of a LIM-Kinase Gene
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Pred. No. 1.8;
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eet, N.W., Suite 701 East
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                                                                                                                                                                                                                                                                                                                                                 Version #1.30
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                              DB 2; Length 792;
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                                                                                                                                                                                                                                                                                                                             RESULT 6
                                                                                                                                                                                                                                                               requence 28, Application US/09117121
Patent No. 6307020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09045764A Patent No. 6127178
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                              NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                               APPLICANT: Hew, Choy
APPLICANT: Gong, Zhiyuan
TITLE OF INVENTION: Intracellular Antifreeze Polypeptides
TITLE OF INVENTION: and Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 1: MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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                                                                   COUNTRY:
                                                                                   CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                               39
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                                                                      TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 0162
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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LENGTH: 39 amino acids
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SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO P
FILING DATE: 30-JAN-1997
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COMPUTER READABLE FORM:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gong, Zhiyuan
TITLE OF INVENTION: Intracellular Antifreeze Polypeptides
TITLE OF INVENTION: and Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 20-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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Pred. No. 0.
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APPLICANT: Michel F. Levesque, M.D.
APPLICANT: Toomas Neuman, Ph.D.
TITLE OF INVENTION: CONVERSION OF NON-NEURONAL CELLS INTO
TITLE OF INVENTION: NEURONS; TRANSDIFFERENTIATION OF EPIDERMAL CELLS
FILE REFERENCE: P07 41494
CURRENT APPLICATION NUMBER: US/09/234,332A
CURRENT FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 238
TYPE: PRT
                                                     CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1813
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                                                                                                                                                    APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
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APPLICANT:
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                    LENGTH: 23
TYPE: PRT
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Human
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Local Similarity 90.9%;
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Local Similarity 90.9%;
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Lodes, Michael A.
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    Mismatches

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                                                   ; TYPE: PRT ; ORGANISM: Rattus norvegicus US-09-360-779-2
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US-09-736-457-1813
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SEQ ID NO 1813
LENGTH: 238
TYPE: PRT
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Best Local (
Query Match
Best Local Similarity
                                                                                                                          SEQ ID NO 2
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Best Local Similarity 90.9%;
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
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APPLICANT:
                                                                                                                                       FILE REFERENCE: CASE-03828
CURRENT APPLICATION NUMBER: US/09/360,779
CURRENT FILING DATE: 1999-07-26
EARLIER APPLICATION NUMBER: 60/094,264
EARLIER FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                         APPLICANT: Deneris, Evan S.
APPLICANT: Fyodoro, Dmitry V.
APPLICANT: Hendricks, Timothy J.
TITLE OF INVENTION: Reagents and Methods for the Screening of Compounds
TITLE OF INVENTION: Useful in the Treatment of Neurological Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
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                                                                                                          LENGTH: 340
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Vedvick, Tom
Carter, Darrick
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Lodes, Michael
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 91.1%;
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Pred. No. 2
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Pred. No. 2.
 Score 41; DB 3; Pred. No. 3.9;
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; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-435-335-2
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US-07-992-288-7
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Sequence 7, Application US/07992288
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SEQ ID NO 2
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                                                                                                                                                   Query Match
Best Local Similarity
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Patent No. 6221355
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                   APPLICANT: Dowdy, Steven F.

TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
FILE REFERENCE: 48881/1742
CURRENT APPLICATION NUMBER: US/09/208,966
CURRENT FILING DATE: 1998-12-10
EARLIER APPLICATION NUMBER: 60/082,402
EARLIER FILING DATE: 1998-04-20
EARLIER FILING DATE: 1998-04-20
EARLIER APPLICATION NUMBER: 60/069,012
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CURRENT FILING DATE: 1999-11-05
EARLIER APPLICATION NUMBER: 09/360,779
EARLIER FILING DATE: 1999-07-26
NUMBER OF SEQ ID NOS: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Deneris, Evan S.
APPLICANT: Fyodoro, Dmitry V.
APPLICANT: Hendricks, Timothy J.
                                                                                                                                                                                                                             LENGTH: 11
TYPE: PRT
                                                                                                                                                                                                               ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 AAAAAAAAAAQ 259
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                                                                                                                                                    Score 40;
Pred. No.
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Pred. No.
                                                                                                                                     Mismatches
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0.19;
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; GENERAL INFORMATION:
; APPLICANT: Lebel, N
; APPLICANT: Eichler
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Query Match
Best Local Similarity 100.0%;
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INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: HOOVER, Allen J.
REGISTRATION NUMBER: 24,103
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/645,121
FILING DATE: 24-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
TM//7/007 368
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
TITLE OF INVENTION: APPARATUS FOR MAKING MULTIPLE SYNTHESIS TITLE OF INVENTION: OF PEPTIDES ON SOLID SUPPORT NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
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Stierandova, Alena
Kalousek, Jan
Bolf, Jan
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Kalousek, Jan
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CORRESPONDENCE Dresser, Goldsmith, Shore & Milnamow, Ltd.
STREET: 180 No. 5342585th Stetson, Suite 4700
CITY: Chicago
STATE: 1.
COUNTRY: USA
ZIP: 60601
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C;Date: 16-Jul_1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000
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finger protein - f	spalt protein - fr	calcium-activated	stripe a/b protein	potassium channel	dachshund protein		dachshund protein	dachshund isoform	elastin precursor	elastin precursor	Cl4orf4 protein -	tropoelastin - she	glucan 1,4-alpha-g	elastin precursor,	T-box protein 2 -

ALIGNMENTS

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A;Cross-references: GB:M98269; NID:g155702; PIDN:AAA27738.1; PID:g155703 A;Note: sequence extracted from NCBI backbone (NCBIN:117102, NCBIP:117104) C;Keywords: neuropeptide
                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-435 <SCH>
                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 267, 22534-22541, 1992
A;TICTS: Identification of a novel type of processing sites in the precursor for the A;Reference number: A44308; MUID:93054550; PMID:1429603
A;Accession: A44308
                                                                                                                                                                                                                                                                                                                                                                                          R;Schmutzler, C.; Darmer, D.; Diekhoff, D.; Grimmelikhuijzen, J. Biol. Chem. 267, 22534-22541, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                        Antho-RFamide precursor - sea anemone (Anthopleura elegantissima)
C;Species: Anthopleura elegantissima
C;Species: Anthopleura elegantissima
C;Date: (O-Jun-1993)#sequence revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A44308
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A;Residues: 1-220 <TAN>
A;Cross-references: DDBJ:D87735; NID:g1620021; PIDN:BAA13443.1; PID:g1620022
C;Superfamily: rat ribosomal protein L14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: JC5954
R;Tanaka, M.; Tanaka, T.; Harata, M.; Suzuki, T.; Mitsui, Y.
R;Tanaka, M.; Tanaka, T.; Harata, M.; Suzuki, T.; Mitsui, Y.
Biochem. Biophys. Res. Commun. 243, 531-537, 1998
A;Title: Triplet repeat-containing ribosomal protein L14 gene in
A;Reference number: JC5954; MUID:98153799; PMID:9480843
A;Accession: JC5954
A;Status: preliminary
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Pred. No. 7.3;
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A;Residues: 1-453,483-617,651-792 <FAZ>
A;Cross-references: EMBL:M36860; NID:g182061; PIDN:AAA52382.1; PID:g182062
A;Cross-references: EMBL:M36860; NID:g182061; PIDN:AAA52382.1; PID:g182062
A;Note: this sequence represents a composite of several splice forms
R;Fazio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenbloom, J.;
R;Fazio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rosenbloom, J.;
Lab. Invest. 58, 270-277, 1988
A;Title: Isolation and characterization of human elastin cDNAs, and age-associated variants of the composition of the c
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R;Fazio, M.J.; Olsen, D.R.; Kauh, E.A.; Baldwin, C.T.; Indik, Z.; Ornstein-Goldstein, N
J. Invest. Dermatol. 91, 458-464, 1988
A;Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recombinant
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R;Bashir, M.M.; Indik, Z.; Yeh, H.; Ornstein-Goldstein, J. Biol. Chem. 264, 8887-8891, 1989
A;Title: Characterization of the complete human elastin A;Reference number: A33705; MUID:89255358; PMID:2722804
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A; Residues: 1-27 <BAS>
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A; Accession:
                                                                                                                                                                                                       C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision
C;Accession: #34516
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A;Residues: 164-453,483-500,507-617,651-792 <FA2>
A;Cross-references: GB:M24782; NID:g182063; PIDN.AAA53190.1; PID:g182064
C;Comment: The term tropoelastin refers to a soluble precursor form of th
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                                                                                                                                                                                                                                                                                                                                         hypothetical protein ZK783.4 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine;1-26/Domain: signal sequence #status predicted <SIG>;27-792/Product; elastin #status predicted <MAT>
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Date: 22-Jun-1990 #sequence revision 26-Jul-1996 #text_change 22-Jun-1999;
Accession: A32707; A33705; A30524; A53891
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Map position: 7q11.23-7q11.23
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DNA Res. 5, 309-31, DNA Res. 5, 309-31, Essu
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C; Date: 16-Jul-1999 #sequence
C; Accession: JE0306
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A;Matrons: 248/3; 373/3; 547/1; 593/2; 905/2; 1042/3; 1116/3; 1317/2; 1376/1 C;Superfamily: bromodomain homology F;1284-1339/Domain: bromodomain homology <BRO>
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A;Residues: 1-1430 <FAV>
A;Cross-references: EMBL:Ul3646; PIDN:AAC24421.1; GSPDB:GN00021; CESP:ZK783.4
A;Experimental source: strain Bristol N2; clone ZK783
C;Genetics:
                                                                                                                                                                  C;Accession: G01855
R;Kiesling, T.L.
submitted to the EMBL Data Library, June
A;Reference number: G08632
A;Accession: G01855
                                                                                                                                                                                                                                                                                           RESULT
G01855
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A; Residues: 1-161 < RIG>
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                                                                                         C; Superfamily: transcription repressor Id-2
                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997
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                                                                                                        A;Molecule type: mRNA
A;Residues: 1-161 <KIE>
A;Cross-references: EMBL:U28368; NID:g881545; PIDN:AAA73923.1;
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Juma lan Ib'

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C.Accession: G96780

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, R ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Reference and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: G96780
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C;Date: 07-Oct-1994 #sequence revision 07-Oct-1994 #text_change 24-Nov-1999
C;Accession: S43260; S37199
R;Riechmann, V.; van Cruechten, I.; Sablitzky, F.
Nucleic Acids Res. 22, 749-755, 1994
A;Title: The expression pattern of Id4, a novel dominant negative helix-loop-helix prote A;Reference number: S43260; MUID:94188125; PMID:8139914
A;Accession: S43260
                                                                                                                                                                                               RESULT 9
T47641
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: rybiv...
A; Map position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X75018; NID:g402637; PIDN:CAA52926.1; PID:g402638 C;Superfamily: transcription repressor Id-2 F;64-106/Region: helix-loop-helix #status predicted
                                                          R; Mewes, H.W.; Rudd, S.; Lemcke, K.; submitted to the Protein Sequence Date
                                                                                                     C;Accession: T47641
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A;Accession: T47641
A;Status: preliminary
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                                        Reference number: Z24470
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Best Local
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Similarity 90.9%;
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ewar, K.;
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C;Species: Drosophila melanogaster
(;Date: 21-Sep-1993 #sequence revision 25-Apr-1997 #text_change 17-Oct-1997
C;Accession: A46221, S22026
R;Barker, D.D.; Wang, C.; Moore, J.; Dickinson, L.K.; Lehmann, R.
Genes Dev. 6, 2312-2326, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Bang, A.G.; Posakony, J.W. Genes Dev. 6, 1752-1769, 1992
A;Title: The Drosophila gene Hairless encodes a novel basic A;Reference number: A44067; MUID:92387549; PMID:1516831
A;Accession: A44067
A;Title: Pumilio is essential for function A;Reference number: A46221; MUID:93093466; A;Contents: embryo
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Mech. Dev. 38, 143-156, 1992
A;Title: Hairless, a Drosophila gene involved in neural
A;Reference number: S33412; MUID:93041287; PMID:1419850
A;Accession: S33412
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                                                                                                                                                                         abdominal segment formation protein pumilio -
                                                                                                                                                                                                                           RESULT 11
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A; Residues: 1-1077 < PF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 19-1077 <BAN>
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A;Introns: 28/2; 51/3; 252/3; 312/3; 350/3; 370/2; 392/3; 410/1; 441/1; 469/1; 604/3; 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-150,'A',152-701,'LL',704-890,'R',892-963,'RLLP',968-973,975-1077
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Cross-references: EMBL:X67239; GB:S49642; NID:g578331;
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R;Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.; Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A;Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-A;Reference number: AB1455; MUID:99178987; PMID:10077609
A;Accession: A81461
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A;Residues: 1-1533 <BAR'S
A;Cross-references: GB:L07943; NID:g158190; PID:g158191
A;Cross-references: GB:L07943; NID:g158190; PID:g158191
NIMOTA: RAGUENCE extracted from NCBI backbone (NCBIN:120203, NCBIP:120204)
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A;Molecule type: DNA
A;Residues: 1-1607 <PYL>
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C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000
C;Accession: A81461; T02837
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A;Residues: 1-361,'A',363-1102,'R',1104-1405,'KN',1408-1495,'V',1497-1518,'S',1520-1533
A;Cross-references: EMBL:X62589; NID:g8393; PID:g8394
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A; Accession: S22026
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A; Residues: 1-153
                                                                                                                                                R;Sezutsu, H.; Tamura, T.; Yukuhiro, K. submitted to the EMBL Data Library, August 1998 A;Description: Characterization of the full length
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A;Experimental source: strain MHOM/IL/81/Friedlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: FlyBase:FBgn0003165
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A;Cross-references: EMBL:AF083334; NID:g3450882; PID:g3450883; PIDN:AAC32606.1
C;Genetics:
                                                                                                                                                                                                                                                                                       fibroin - Chinese oak silkmoth
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C;Species: Leishmania major
                                         A;Residues: 1-2639
                                                         ;Status: preliminary; translated;Molecule type: DNA
                                                                                                       ;Accession: T31328
                                                                                                                           Reference number: Z20995
                                                                                                                                                                                                                                     ;Species: Antheraea pernyi (Chinese oak silkmoth);Date: 22-Oct-1999 #sequence_revision 22-Oct-1999
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A;Title: Evolution of homeotic gene regulation and function in flies
A;Reference number: S58850; MUID:95075456; PMID:7840822
                                                                                                                                                                                                                                                                                                                                                                                             antifreeze protein precursor - yellowtail flounder C;Species: Limanda ferruginea (yellowtail flounder) C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:L42137
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, C;Superfamily: unassigned homeobox proteins; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Warren, R.W.; Nagy, L.; Selegue, J.; Gates, J.; Carroll, Nature 372, 458-461, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homeotic protein ultrabithorax homolog - Junonia coenia (fragment)
N;Alternate_names: ultrabithorax homeodomain protein
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                                                                                                                                                                                                      A;Cross-references: EMBL:X06356; NID:g64041; A;Note: part of this sequence, including the C;Superfamily: antifreeze protein
                                                                                                                                                                                                                                                                                                              Eur. J. Biochem. 168, 629-633, 1987
A; Title: Structural variations in the alanine-rich antifreeze A; Reference number: S02376; MUID:88029483; PMID:3665937
                                                                                                                                                                                                                                                                                                                                                             C;Accession: S02376
R;Scott, G.K.; Davies, P.L.; Shears, M.A.; Fletcher, G.L.
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A; Residues: 1-40 < WAR
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A; Residues: 1-97 <SCO>
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                                                                                                                                       F;49-96/Product: antifreeze protein #status
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 GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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ZP12 BRARE
PO33 BRARE
PO31 RAT
IX33 MOUSE
TRX3 HUMAN
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SMART; SM00132; LIM; 2.
SMART; SM00132; LIM DOMAIN 1;
PROSITE; PS00478; LIM DOMAIN 2;
PROSITE; PS50023; LIM DOMAIN 2;
PROSITE; PS00027; HOMEOBOX 1; 1.
                                                                                                                  the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entitles requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
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SMART; SM00389;
SMART; SM00132;
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Mammalia; Eutheria; Rodentia;
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28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99162575; PubMed=10051612;
Rincon-Limas D.E., Lu C.-H., Canal I., Calleja M.,
Rodriguez-Esteban C., Izpisua-Belmonte J.C., Botas J.;
"Conservation of the expression and function of apterous orthologs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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ling; Zinc; Transcription regulation.
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A -> TR (IN REF. 1).

GHEPHSPSQTTLTINLF -> AMSLTAPHKRLLPTFSNDSQP
PHPTISLKKKLSLV (IN REF. 1).

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AKSEAPA -> QERGSR (IN REF. 1).
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                   Anthopleura elegantissima (Sea anemone).

Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia;
Nynantheae; Actiniidae; Anthopleura
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PROSITE; PS0023; LIM DOMAIN 2;
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
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Pfam; PF00046; homeobox; 1.
Pfam; PF00412; LIM; 2.
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GO; GO:0007498; P:mesoderm devel
GO; GO:0007399; P:neurogenesis;
InterPro; IPR001356; Homeobox.
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from sea anemonee.";
Proc. Natl. Acad. Sci. U.S.A. 83:9817-9821(1986).
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MEDLINE=87092339; PubMed=2879288;
Grimmelikhuijzen C.J.P., Graff D.;
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                                                                                                                                                                                                                                                 "Identification of a novel type of processing sites in the precursor for the sea anemone neuropeptide Antho-RFamide (<Glu-Gly-Arg-Phe-NH2) from Anthopleura elegantissima.";
1. Biol. Chem. 267:22534-22541(1992).
                                                                                                                                                                                                                                                                                                       MEDLINE=93054550; PubMed=1429603; Schmutzler C., Darmer D., Diekhoff D.,
                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1993 (Rel. 27, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6110;
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                                                                                                                                                                                    "Isolation of pyroGlu-Gly-Arg-Phe-NH2
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                                                                                                                            FUNCTION: NOT KNOWN BUT IT NEUROMUSCULAR SYNAPSES.
                                                                                                                   SUBCELLULAR LOCATION:
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EMBL; M98269; AAA27738.1;

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AC P15502; Q14233; Q14238;

DT 01-APR-1990 (Rel. 14, Last sequence updat

DT 15-SEP-2003 (Rel. 42, Last annotation upr

Elastin precursor (Tropoelastin).
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Mammalia; Eutheria;
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nilarity 100.0%;
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 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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EMBL; M17282; EMBL; M16983; EMBL; M17265; EMBL; M17266; EMBL; M17267; EMBL; M17267;

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between
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Jinvest. Dermatol. 91:458-464(1988).

TISSUE-Placenta;

TISSUE-Placenta;

TISSUE-Placenta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "LIM-kinasel hemizygosity implicated in impaired visuospatial constructive cognition."; Cell 86:59-69(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Frangiskakis J.M., Ewart A.K., Morris C.A., Mervis C.B., Bertrand J., Robinson B.F., Klein B.P., Ensing G.J., Everett Green B.D., Proeschel C., Gutowski N.J., Noble M., Atkinson I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Hippocampus, and Placenta; MEDLINE=96291399; PubMed=8689688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M., Rosenbloom J., Uitto J.;
"Isolation and characterization of human elastin cDNAs, and ageassociated variation in elastin gene expression in cultured skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISC
TISSUE=Skin fibroblast;
MEDLINE=89009960; PubMe
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(117)
**SEQUENCE FROM N.A. (ISOFORM B).
**MEDLINE=87289668; PubMed=3039501;
Indik Z., Yeh H., Ornstein-Goldstein N.,
Rosenbloom J.C., Peltonen L., Rosenbloom
                                                                                                                                                                                                                                 modified
                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Odelberg S.J.,
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                                                                                                                                                                                                   entities
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                                                                                                                                                                                                                                                                                                                                                                         IsoId=P15502-2; Sequence=VSP 004243; PTM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS. PISASE: Haploinsufficiency of ELN may be the cause cardiovascular and musculo-skeletal abnormalities ob Williams-Beuren syndrome (WBS), a rare developmental is a contiguous gene deletion syndrome involving gen chromosome band 7q11.23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2; Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P15502-1; Sequence=Displayed;
                                                                                                                                                                                                                           non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                      requires a
                                                                                                                                                                           equires a license agreement (S email to license@isb-sib.ch).
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EMBL; M17272; AAC98394.1; J
EMBL; M17273; AAC98394.1; J
EMBL; M17275; AAC98394.1; J
EMBL; M17276; AAC98394.1; J
EMBL; M17276; AAC98394.1; J
EMBL; M17278; AAC98394.1; J
EMBL; M17279; AAC98394.1; J
EMBL; M17279; AAC98394.1; J
EMBL; M17280; AAC98394.1; J
EMBL; M17281; AAC98394.1; J
EMBL; M24782; AAA52382.1; -
EMBL; M24782; AAA52382.1; -
EMBL; M26292; AAB17544.1; -
EMBL; X15603; AAB33627.1; -
EMBL; X15603; AAB31627.1; -
EMBL; A32707; EAHU.
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P47928; Q13005;
01-FEB-1996 (Re)
01-FEB-1996 (Re)
15-SEP-2003 (Re)
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MIM; 194050;
MIM; 194050;
GO; GO:000557
GO; GO:000520
GO; GO:000828
GO; GO:000801
GO; GO:000758
InterPro; IPR
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CHAIN
DISULFID
                             MEDLINE=99087490; PubMed=9872455;
Rigolet M., Rich T., Gross-Morand
Viegas-Pequignot E., Junien C.;
                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
           "cDNA cloning, tissue
the human ID4 gene.";
                                                                 SEQUENCE FROM N.A.
                                                                                      TISSUE=Abdominal adipose tissue;
Kiesling T.L., Christy B.A.;
Submitted (JUN-1995) to the EMBL
                                                                                                                       SEQUENCE
                                                                                                                                                                                                  DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Williams-Beuren syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01500;
Structural protei
                                                                                                                                          NCBI_TaxID=9606;
human
Res. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO:0005578; C:extracellular matrix; TAS.
GO:0005615; C:extracellular space; TAS.
GO:0005201; F:extracellular matrix structural constituent;
GO:000823; F:cell proliferation; TAS.
GO:0008015; P:circulation; TAS.
GO:0007397; P:histogenesis and organogenesis; TAS.
GO:0007585; P:respiratory gaseous exchange; TAS.
                                                                                                                                                                                                                                                                                                                302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGNC:3327;
                                                                                                                                                                                                                                                                                                                                                                     Similarity
n ID4 gene.";
5:309-313(1998)
                                                                                                                                                                                                                                                                                                                                   AAAAAAAAAK 11
                                                                                                                                                                                                                                                                                                                AAAAAAAAAK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR003979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                                                                     730
                                                                                                                                                                                                 (Rel. 33, Created)
(Rel. 33, Last sequence up
(Rel. 42, Last annotation
protein inhibitor ID-4.
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                     N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                          STANDARD;
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730
725
477
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                     distribution
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                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                    ELASTIN.
BY SIMILARITY.
Missing (in isoform 2).
/FTId=VSP 004243.
W; AB06D15BA567AE46 CRC64;
                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                       EMBL/GenBank/DDBJ
                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                       and
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on update)
                                                                                                                                                                                                                                                          161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Repeat;
splicing.
                     chromosomal localization
                                            Molina-Gomes
                                                                                                                                                                                                                                                                                                                                                                                DB
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Bind N.N.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hoigh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Biromstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Wilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-95394461; PubMed=7665172;
MEDLINE-95394461; PubMed=7665172;
Medlecular cloning of ID4, a novel domina
T human gene on chromosome 6p21.3-p22.";
Genomics 27:200-203(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.L., Feingold E.A., Grouse L
Klausner R.D., Collins F.S., Wagner L.,
Altschul S.F., Zeeberg B., Buetow K.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Mashreghi-Mohammadi
Submitted (DEC-1998)
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dominant negative helix-loop-helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L.H., Derge J.G.,
, Shenmen C.M., Schuler G
, Schaefer C.F., Bhat N.K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Usage by and for http://www.isb-sib.
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CONFLICT CONFLICT Nuclear DOMAIN DOMAIN DOMAIN EMBL; U28368; AAA73923.1; -.
EMBL; Y07958; CAA69255.1; -.
EMBL; U16153; AAA82882.1; -.
EMBL; AL022726; CAA18779.1; MIM; PROSITE; PS00038; HLH_1; PROSITE; PS50888; HLH_2; GO; GO:0003714; F:transcription GO; GO:0006357; P:regulation of EMBL; BC0149' PIR; G01855; SMART; Pfam; PF00010; HLH; 1. Genew; [nterPro; 600581; AL022726; CAA18779.1; -. BC014941; AAH14941.1; -. SM00353; HLH; 1. HGNC:5363; ID4. protein IPR001092; 39 118 10 39 77 G01855 48 105 124 14 40 79 HLH_basic. ٠٠ POLY-ALA.

HELIX-LOOD-HELIX MOTIF (
POLY-PRO.

SGRKA -> RPLR (IN REF. 3)

AA -> Q (IN REF. 3). co-repressor activity; transcription from Pol (IN REF. 3) (BY SIMILARITY). pro.

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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUSE
                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restu use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=99051333; PubMed=9831657;
Mantani A., Hernandez M.C., Kuo W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Last sequence 16-OCT-2001 (Rel. 40, Last annotati DNA-binding protein inhibitor ID-4. ID4 OR ID4 OR IDB4 (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
        TRANSFAC; T01658; --
MGD; MGI:99414; Idb4.
MGD; MGI:99414; Idb4.
InterPro; IPR001092; HLH_basic.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
                                                                                                                                                    entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   helix protein, is distinct from Id1, Nucleic Acids Res. 22:749-755(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                EMBL; AJ001972; CAA05120.1; -.
EMBL; AF077859; AAD05213.1; -.
PIR; S43260; S43260.
                                                                                                                                                                                                                                                                                  :-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structure, chromosomal localisation and expression of the murine dominant negative helix-loop-helix Id4 gene."; Biochim. Biophys. Acta 1443:55-64(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Riechmann V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99057583; PubMed=9838043;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                        EMBL; X75018; CAA52926.1; -.
                                                                                                                                                                                                                                                                                                                                                                                              Mantani A., Hernandez M.C., Ku
"The mouse Id2 and Id4 genes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94188125; PubMed=8139914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Riechmann V., van Cruechten I., Sablitzky F.;
"The expression pattern of Id4, a novel dominant negative helix-loop-
nelix protein, is distinct from Id1, Id2 and Id3.";
                                                                                                                                                                                                                                                                                                                                                                                  ocalization.
                                                                                                                                                                                                                                                                                           e 222:229-235 (1998).

FUNCTION: ID (INHESTOR OF DNA BINDING) HLH PROTEINS DNA-BINDING DOMAIN BUT ARE ABLE TO FORM HETERODIMERS HLH PROTEINS, THEREBY INHIBITING DNA BINDING.

SUBUNIT: HETERODIMER WITH OTHER HLH PROTEINS.

SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cruechten I., Cinato E., Fox M., chmann V., Sablitzky F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. "ID" SUBFAMILY.
                                                                              S43260; S43260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39
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(Rel. 31, Last sequence update)
(Rel. 40, Last annotation update)
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Pred. No.
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Nuclear protein.
DOMAIN 39
DOMAIN 65
DOMAIN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and SOX21; and SOX3.";
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30-MAY-2000 (Rel.
15-SEP-2003 (Rel.
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                                                                                                                                               PROSITE; PS50118; HMG_BOX_2; 1.

Transcription regulation; Repressor; DNA-binding; Nuclear DNA_BIND 8 76 HMG_BOX.
                                                                                                                                                                                                                                                                                                                   MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MRDLINE-99373261; PubMed=10441749;
Malas S., Duthie S., Deloukas P., Episkopou V.;
Mele isolation and high-resolution chromosomal mapping
and SOX21; two members of the SOX gene family related t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              094651;
                                                                                                                                                                                                               SMART; SM00398; HMG;
                                                                                                                                                                                                                                  GO; GO:0003702; F:RNA polymerase II transcription factor acti. GO; GO:0006357; P:regulation of transcription from Pol II pro. InterPro; ITRR009010; HMG 12_box. Pfam; PF00505; HMG_box; T.
                                                                                                                                                                                                                                                                                                                                       TRANSFAC; T04921; Genew; HGNC:11197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
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                                                                                                                                                                                                                                                                                                                                                                                  HSSP; Q05066;
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF107044; AAC95381.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Iranscription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: ACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
SUBCELLULAR LOCATION: Nuclear (Potenti
SIMILARITY: Contains 1 HMG box domain.
                                                                                                                                                                                                                                                                                                                   604974; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions of the long as its content is in no war by non-profit institutions of the long as its content is in no war by non-profit institutions of the long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is not as long as long as its content is not as long as l
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    AAAAAAAAAAK 11
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161 AA;
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105
124
                                                                                                                                28580 MW;
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90.9%;
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Pred. No.
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Pred. No.
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L; Mismatches
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HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
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                                                                                                                                99DC899B7EC9A96B
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                                                                                       Length 276;
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                                                                                                                                CRC64;
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DAFFEE BROSSON
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SX21_CHICK
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Best Local S
Matches 10
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15-JUL-1998
15-JUL-1998
15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Uchikawa M., Kamachi Y., Kondoh H.;
"Two distinct subgroups of Group B Sox genes
activators and repressors: their expression of the control o
                                                                                                                                                                                                                            MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organogenesis of the chicken."; Mech. Dev. 84:103-120(1999).
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15-SEP-2003
              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99400103; PubMed=10473124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., FUNCTION,
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                                                                                                Zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Acts as a negative regulator of transcrisuBCELLULAR LOCATION: Nuclear (Potential).
TISSUE SPECIFICITY: Expressed predominantly in CNS
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                                                                                                                                                                                                         MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00505; HMG
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SM00398; HMG; 1.
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(Rel. 42, Last a
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                                                                                                                                                                                                         STANDARD;
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                                                                                     36, Created)
36, Last sequence update)
42, Last annotation update)
in ZIC 2 (Zinc finger protein
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146
166
187
223
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Weognathae; Galliformes; Phasianidae; Phasianinae;
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HMG BOX
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POLY-SER.
POLY-ALA.
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                 Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                         PRT;
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                   Muridae;
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                                                                                                    of.
                                                                                                  the
                 Euteleostomi;
; Murinae; Mus.
                                                                                                  cerebellum
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Best Local
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Q24708;
15-SEP-2003
15-SEP-2003
15-SEP-2003
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HSSP; P08047; 1SP2.
TRANSFAC; T04670; -.
MGD; MGI:106679; Zic2.
GO; GO:0007417; P:central nervous system development;
GO; GO:0077417; Znf_C2H2.
TherPro; IPR007087; Znf_C2H2.
                                                                                                                                                                                                                                                                              DOMAIN
ZN_FING
ZN_FING
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DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as modified and this statement is not removed. Use this requires a license agreement (See htt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 271:1043-1047(1996).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: CNS. A HIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
TISSUE=Cerebellum;
MEDLINE=96132843; PubMed=8557628;
    Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosop
NCBI TaxID=7244;
                                                             CSW.
                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00355; ZnF CZH2; 4.

PROSITE; PS00028; ZINC FINGER C2H2_1; 3.

PROSITE; PS50157; ZINC FINGER C2H2_2; 4.

Zinc-finger; Metal-binding; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aruga J., Nagai T., Tokuyam
Chapman V.M., Mikoshiba K.;
                                     Eukaryota;
                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS
                                                                      Protein-tyrosine phosphatase corkscrew
                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 4 C2H2-type zinc fingers.
                                                  Drosophila
                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mouse zic gene family. Homologues
                                                                                                                                                                               458
                                                                                                                                                                                                                          10;
                                                                                                                                                                                                     1 AAAAAAAAAAK 11
                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                               AAAAAAAAAAR
                            Metazoa; Arthropoda; Hexapoda; Insecta;
Endopterygota; Diptera; Brachycera; Musc
                                                  virilis (Fruit fly).
                                                                                (Rel. 42, Created)
(Rel. 42, Last sequence up
(Rel. 42, Last annotation
                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                    A,
                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                        23
97
231
231
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                                                                                                                                                                                                                                    93.3%;
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                                                                                                                                                                                                                                                                                       C2H2-TYPE
C2H2-TYPE
C2H2-TYPE
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POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                 POLY-ALA.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A HIGH LEVEL
                                                                                                                                                                                                                           Pred. No. 14;
; Mismatches
                                                                                                                                                                                                                                              Score 42;
                                                                                                                                                                                                                                                                               POLY-ALA
                                                                                                                                                                                                                                                                                                                                           POLY-HIS
                                                                                                                                                                                                                                                                                                                                                        POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                      POLY-HIS
                                                                                                                            PRT;
                                                                                                                                                                                                                                                                    0065BD75B52E7DD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki Y., Okazaki
                                                                                             update)
                                                                       update)
w (EC 3.1.
                                                                                                                             764
                                                                                                                                                                                                                                     DB 1;
14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the Drosophila pair-rule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no restrictions on no as its content is in no
                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                 Repeat; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                    (ATYPICAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            its content
Usage by an
                              Muscomorpha
                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                               Length 530;
                                                                        .3.48)
                                         Pterygota;
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                                                                        (Fragment)
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"The role of the Drosophila corkscrew protein as a transducer
downstream of receptor tyrosine kinases is functionally conserved.";

RT downstream of receptor tyrosine kinases is functionally conserved.";

RI Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.

CC :- FUNCTION: Required in all receptor tyrosine kinase signaling

CC :- FUNCTION: Functions downstream of the receptor tyrosine kinase

CC torso, acting in concert with D-Raf via tailless. Also functions

CC downstream of Egfr (epidermal growth factor receptor) and btl

CC (fibroblast growth factor receptor). The SH2 domain suggests that

CC (fibroblast growth factor receptor). The SH2 domain suggests that

CC csw effects its role by mediating heteromeric protein

CC (interactions. Maternally required for normal determination of cell

CC fates at the termini of the embryo. Required for cell fate

CC specification of the ventral ectoderm, in the developing embryonic

CC consisted development for proper formation. Functions during

CC imaginal development for proper formation of adult structures such
                                                                                                          Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00017; SH2; 1.

Pfam; PF00102; Y_Phophatase; 1

PRINTS; PR00700; PRTYPHPHTASE.

PRINTS; PR00401; SH2DOMAIN.

Pr0Dom; PD00401; SH2; 1.

SMART; SM00194; PTPC; 1.

SMART; SM00252; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for com
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                      DOMĀIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50001; SH2; 1.
PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR PHOSPHATASE 2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000980; SHz.
InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000242; Tyr_PP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U22356; AAB02545.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0016496; Dvir\csw.
InterPro; IPR000980; SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tyrosine + phosphate.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE
SIMILARITY: BELONGS TO THE NON-RECEPTOR THAT CONTAINS S
TYROSINE PHOSPHATASE FAMILY. SUBCLASS THAT CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains at least 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q06124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eyes, aristae, L5 wing vein and the tarsal claw
                                                                                                                                       Similarity
                                                  AAAAAAAAAAK 11
                                                                                                             Conservative
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325
460
191
281
281
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616
690
753
                                                                                                                                                                                                                          761
82125
                                                                                                                                    93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Developmental protein.
                                                                                                                                                                                                                          MW ;
                                                                                                                                                                                                                                                                            ALA-RICH.
POLY-ASN.
SER-RICH.
POLY-GLN.
ALA-RICH.
                                                                                                                                    Score 42; DB
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN-TYROSINE PTPASE INSERT (CY BY SIMILARITY.
                                                                                                                                                                                                                          66008EA8560A2F7D CRC64;
                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CYS/SER-RICH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Usage
                                                                                                          <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHATASE
                                                                                                                                                               Length 764;
                                                                                                                Indels
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                                                                                                             Gaps
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RESULT 11
HLES_DROME
       RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Brandon R.C., Rogers V.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Haridon R.C., Rogers V.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Haril J.F., Agbayani A., An H.-J., Andrews-Pfamnkoch C.R., Miklos G.L.G.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktarogju L., Beasley E.M.,

RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Butler H., Caddeu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Chery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Chery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Duzbin K.J., Bvangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hermandez J.R., Houck J.,

RA Harris N.L., Matvey D., Helman T.J., Hermandez J.R., Houck J.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Mount S.M., Moly M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Mount S.M., Pelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Mount S.M., Pelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA Sylskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

"The genome sequence of Drosophila melanogaster.",

CC. Parters B.M., Shool B.M., Robin B. M., Schen H.O.,

RA Globe R.A., Myers B.W., Zhon M., Zhann G., Zhan G., Zheng L.,

Schence 287:2185-2195 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLES DROME STAN
Q02308; Q9VDKO; Q9V
01-FEB-1994 (Rel. 2
01-FEB-1994 (Rel. 2
15-SEP-2003 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mecn.
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"The Drosophila gene Hairless encodes a novel basic protein that controls alternative cell fates in adult sensory organ development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hairless protein.
H OR CG5460.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maier D., Stumm G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=92387549; PubMed=1516831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEDLINE=93041287; PubMed=1419850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ss, a Drosophila gene involved
    serine rich protein.";
vv. 38:143-156(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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A POTENT ANTAGONIST OF NEUROGENIC
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EMBL; X67239; CAA47664.1; -.
EMBL; AB003731; AAF55790.1; -.
EMBL; AB003731; AAF55791.1; -.
EMBL; AB003731; AAF55791.1; -.
EMBL; AA4067; A44067.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0001169; H.
GO; GO:0003714; F:transcription co-repressor activity;
GO; GO:0007219; P:N receptor signaling pathway; NAS.
GO; GO:0008052; P:sensory organ determination; IMP.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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between the Swiss Institute of Bioinformatics and the EMBL
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TISSUE SPECIFICITY: OVARY, EMBRYOS, LARVAL
DISCS.
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SUBCELLULAR LOCATION: Nuclear (Probable).
ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
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PIR; A46221; A46221.
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Barker D.D., Wang C., Moore J., Dickinson L.K.,
"Pumilio is essential for function but not for or
Drosophila abdominal determinant Nanos.";
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Pfam; PF00806; PUF; 8.
SMART; SM00025; Pumilio;
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GO; GO:0008258; P:head inv
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MEDLINE=92249205; PubMed=1576962;
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ES DEV. 6:2312-2326(1992).

ES DEV. 6:2312-2326(1992).

ETMOTION: PUM IS THE ONLY GENE REQUIRED FOR NOS ACTIVITY THAT FUNCTION: PUM IS THE ONLY GENE LOCALIZATION OF GERM LINE DETERMINANTS. PUM IS REQUIRED DURING EMBRYOGENESIS WHEN NOS ACTIVITY APPARENTLY MOVES ANTERIORLY FROM THE POSTERIOR POLE SUBCELLULAR LOCATION: CYTOPLASMIC. IT IS CONCENTRATED IN THE CORTICAL REGION OF THE EMBRYO BENEATH THE NUCLEI.

DEVELOPMENTAL STAGE: EXPRESSED IN THE OVARIES AND DURING THE
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an email to license@isb-sib.ch).
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01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Achaete-scute homolog 1 (Mash-1).
ASCL1 OR ASH1 OR MASH1 OR MASH-1.
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Limanda ferruginea (Yellowtail flounder).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Pleuronectidae; Limanda.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1988 (Rel. 09, Last sequence update)
01-AUG-1990 (Rel. 15, Last annotation update)
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SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALANINE-RICH, AMPHIPHILIC AND ALPHA-HELICAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      937
                                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S02376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biochem.
                                                                                                                                                                                                                                                                                                                                            57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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IPR000104; Antifreeze_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97
8865 MW;
                  Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48
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Pred. No. 5.
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ANTIFREEZE PROTEIN.
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                                                                                                                                  update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 97;
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                                              Best
                                Matches
                                                          Query Match
                                                                                                                                PROSITE;
Neurogenesis; L...
Nuclear protein.
Nuclear protein.
30
47
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                                                                                                      DNA_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning, sequencing and expression of the mouse mammalian achaete-scute homolog 1 (MASH1).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE PROM N.A.
MEDLINE=93144349; PubMed=8424959;
del Amo F., Gendron-Maguire M., G
                                                                                          SEQUENCE
                                                                                                                                                                                           SMART; SM00353; HLH; 1.

PROSITE; PS00038; HLH_1; 1.

PROSITE; PS50888; HLH_2; 1.
                                                                                                                                                                                                                                                                   MGD; MGI:96919; Ascll.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0007400; P:neuroblast cell
                                                                                                                                                                                                                                                                                                                                                                                                                      agu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guillemot F., Joyner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochim.
                                                                                                                                                                                                                                       Pfam; PF00010; HLH; 1.
                                                                                                                                                                                                                                                                                                               PIR; S28186;
TRANSFAC; T01
                                                                                                                                                                                                                                                                                                                                           EMBL; M95603;
                                                                                                                                                                                                                                                                                                                                                                                                       modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the developing nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94031847; PubMed=8217843;
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                                                                                                                                                                                                                                                        [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dynamic expression of the murine
                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE DEV. 42.1171-185(1993).

FUNCTION: MAY PLAY A ROLE AT EARLY STAGES OF DEVELOPMENT OF SPECIFIC NEURAL LINEAGES IN MOST REGIONS OF THE CNS, AND OF SEVERAL LINEAGES IN THE PNS. ESSENTIAL FOR THE GENERATION OF OLFACTORY AND AUTONOMIC NEURONS. ACTIVATES TRANSCRIPTION BY BINDING TO THE E BOX (5'-CANNTG-3').

SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHLH PROTEIN. FORMS A HETERODIMER WITH E12/E47.

SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY TRANSCRIPTION FACTORS. ASC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.5 ITS EXPRESSION PATTERN CHANGES FROM A RESTRICTED TO A WIDESPREAD ONE, IT IS THEN FOUND AT VARIABLE LEVELS IN THE VENTRICULAR ZONE IN ALL REGIONS OF THE BRAIN. FROM DAY 12.5 TO POST-NATAL STAGES IT IS ALSO EXPRESSED IN CELLS OUTSIDE OF THE VENTRICULAR ZONE THROUGH THE BRAIN, AND IN ADDITION IT IS ALSO EXPRESSED DURING DEVELOPMENT OF THE OLFACTORY EPITHELIUM AND EXPRESSED DURING DEVELOPMENT OF THE OLFACTORY EPITHELIUM AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENTAL STAGE: BETWEEN EMBRYONIC DAYS 8.5 AND 10. FOUND IN THE NEUROEPITHELIUM OF THE MIDBRAIN AND VENTRA FOREBRAIN, AS WELL AS IN THE SPINAL CORD. BETWEEN DAYS 12.5 ITS EXPRESSION PATTERN CHANGES FROM A RESTRICTED T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NATAL STAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEURAL RETINA
   ب
                                10;
                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     non-profit institutions as long and this statement is not removed.
   AAAAAAAAAAK 11
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                                                                                                                                                                                                                                                     IPR001092;
                                                                                                                                                                                                                                                                                                               T01619;
                                                                                       116
127
231 AA;
                                Conservative
                                                                                                                                                                                                                                                                                                                             S28186.
                                                                                                                                                                              Differentiation; Developmental protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                           AAA37780.1;
                                                                                                      43
52
126
166
                                                                                          24755
                                                                                                                                                                                                                                                       HLH_basic
                                               90.9%;
                                                             91.1%;
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                                1:
                                                                               POLY-ALA.
POLY-GIN.
BASIC DOWAIN.
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
F4B4A62052AEBE7 CRC64;
                                               Score 41;
Pred. No.
                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gridley T.;
                                                                                                                                                                                                                                                                      fate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Achaete-Scute homologue
                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                      determination;
                                                             DВ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL outstation
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ASH1_RAT
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                                                                                                                                     Query Match
Best Local S
Matches 10
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                                                                                                                                                   DNA BIND
                                                                                                                                                                                                                                                                                            InterPro; IPR001092; HLH_basic.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                      EMBL; X53725; CAAS. FIR; S11563; S11563.
                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (so or send an email to license@isb-sib.ch).
                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Achaete-scute homolog 1.
ASCL1 OR ASH1 OR MASH-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P19359;
01-NOV-1990
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                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                      Nuclear protein.
                                                                                                                                                                                                                                                          PROSITE; PS00038; HLH_1; 1.
PROSITE; PS50888; HLH_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ÷
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed in neuronal precursors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johnson J.E., Birren S.J., Anderson D.J.; "Two rat homologues of Drosophila achaete-scute specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90363294; PubMed=2392153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                           TRANSFAC; T00484; -.
                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                        Veurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE: IT IS FIRST OBSERVED AFTER NEURULATION, IN 10.5 DAY OLD (E10.5) RAT EMBRYOS, AND IS RESTRICTED TO SUBSETS OF NEUROEPITHELIAL CELLS IN THE SERIAL CORD AND THE BRAIN, BETWEEN E10.5 AND E13.5. IN THE PERIPHERY, ITS EXPRESSION IS RESTRICTED TO SOME LINEAGES OF NEURAL CREST-DERIVED CELLS, NAMELY IN SYMPATHETIC AND ENTERIC NEURAL PRECURSORS. IN THE PNS ITS EXPRESSION IS EXTINGUISHED AT OR BEFORE DIFFERENTIATION.

EXTINGUISHED AT OR BEFORE DIFFERENTIATION.

SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. ASC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHLH PROTEIN. FORMS A HETERODIMER WITH E12/E47.
SUBCELLULAR LOCATION: Nuclear (Probable):
TISSUE SPECIFICITY: DEVELOPING CNS AND PNS AT EMBRYONIC AND POST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UXE 346:858-861 (1990).

FUNCTION: MAY PLAY A ROLE AT EARLY STAGES OF DEVELOPMENT OF SPECIFIC NEURAL LINEAGES IN MOST REGIONS OF THE CNS, AND OF SEVERAL LINEAGES IN THE PNS. ESSENTIAL FOR THE GENERATION OF OLFACTORY AND AUTONOMIC NEURONS. ACTIVATES TRANSCRIPTION BY BINDING TO THE B BOX (5'-CANNTG-3').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NATAL STAGES.
                                                                                                                                                                                                                                                                                                                                                                               X53725; CAA37760.1;
                                                                10;
                                                                                 Similarity
AAAAAAAAAQ 45
                              АААААААААК 11
                                                                Conservative
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                                                                                                                                                                                                                                        Differentiation; Developmental protein; DNA-binding;
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54
128
168
                                                                                                                                   24972 MW;
                                                                                 91.1%;
90.9%;
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Last annotation update)
                                                               Score 41; DB 1;
Pred. No. 11;
L; Mismatches
                                                                                                                                                 POLY-ALA.
POLY-GLM:
BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY)
                                                                                                                                     036BDAC8E2D23274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233
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Perfect score:
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sp_plant:*
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Q8c1r8 mus musculu
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Q8gsb1 oryza sativ
Q1533 homo sapien
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Q14237 rattus norv
Q8ch17 rattus norv
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Q9ftj6 oryza sativ
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Q9cr57 mus musculu	Q9d8q1 mus musculu	Q8h8g6 oryza sativ	mus mu	Q9mbf7 lilium long	manduca	junonia co	ea	σ	Q9w198 drosophila	Q94599 leishmania	Q9vhh4 drosophila		9		o.	N		Q24708 drosophila	Q960w5 drosophila		arabidops	Q967t8 antheraea p	Q93119 antheraea p	Q8s6q8 oryza sativ	oryza sat	Q8vzd2 arabidopsis	-	N

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RESULT 2 Q8CH22 ID Q8CH22 PRELIMINARY; PRT; 171 AA. AC Q8CH22;	2y 1 AAAAAAAAK 11 b 13 AAAAAAAAA 23	Query Match 100.0%; Score 45; DB 11; Length 102; Best Local Similarity 100.0%; Pred. No. 11; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		W Hymothetical protein.		60,770 full-length cDNAs.";	"Analysis of the mouse transcriptome based on functional	the						NCBI TaxID=10090;	Mammalia; Eutheria; Rodentia;	Eukaryota; Me	Mus musculus	domain/type I	Hypothetical a	01-MAR-2003 (01-MAR-2003 (TrEMBLrel.	01-MAR-2003 (TrEMBLrel.	Q8C1R8;	D Q8C1R8 PRELIMINARY; PRT; 102 AA.	RESULT 1
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Last Last

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NCBI_TaxID=10090;

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;

Craniata; Vertebrata; l Sciurognathi; Muridae;

Euteleostomi;
; Murinae; Mus.

Mus musculus (Mouse)

CKT1R1.

protein

SEQUENCE

FROM N.A.

STRAIN=CD-1; TISSUE=Testis; Xu X., Bai X., Silvius D., Escalier D., McFarl Xu X., Bai X., Silvius D., Escalier D., McFarl "Ck2 differentially phosphorylate a family of basic nuclear proteins."; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ

Escalier D., McFarland L., orylate a family of novel s

., Xu P.-X.;
spermatid-specific

AF463500; AAO15673.1; -. VCE 171 AA; 19175 MW;

2482A9F50B121B68 CRC64;

databases.

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l Similarity

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Q8N1Z3;
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Park M., Moon E., Hwang "Molecular cloning of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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     sapiens
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1 protein FLJ37192.
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llarity 100.0%;
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putative
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Pred. No. 37;
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Submitted (JAN-2000)
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Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie
Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,

Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashit
Watsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,

Murakawa K., Kanehori K., Takahashi-Pujii A., Oshima A.,

Sugano S., Nagahari K., Masuo Y., Nagai K., Isogai T.;
"Oryza sativa nipponbare(GA3) clone:OJ1340 CO8."; Submitted (MAY-2002) to the ENEMBL; AP004671; BAC16472.1; -EMBL; AP005292; BAC45222.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative calcium/calmodulin-dependent protein kinase CaMK.
P0524G08.10 OR OJ1340 C08.39.
Oryza sativa (japonica cultivar-group).
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00027; HOMEOBOX 1; 1.

PROSITE; PS50071; HOMEOBOX 2; 1.

PROSITE; PS500478; LIM DOMAIN 1; 2.

PROSITE; PS50023; LIM DOMAIN 2; 2.

PROSITE; PS50023; LIM DOMAIN 2; 2.

PROSITE; PS50558; LIM HOMEODOMAIN; 1.

PROSITE; PS50558; LIM HOMEODOMAIN; 1.

SEQUENCE 397 AA; 43363 MW; D4DB2956EA647F8D C
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                                                                                                                  STRAIN=cv.
Sasaki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8GSB1;
01-MAR-2003
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Mammalia; Eutheria;
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Matsumoto T
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                                                                                                                  Katayose Y.;
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Kimura K., Yamashita H.,
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RESULT 7
015336
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Best Local 9
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SEQUENCE FROM N.A.
Li D.Y., Toland A.E., Boak B.B., At
Morris C.A., Keating M.T.;
"Elastin point mutations cause an (
"Elastin point mutations cause an (
supravalvular aortic stenosis.";
Hum. Mol. Genet. 0:0-0(1997).
EMBL; U93037; AAB65621.1; JOINED.
                                                                                                                                        015336;
015336;
01-JAN-1998
01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                        EXQUENCE TOOL TO A SEA BOOK B.S., Morris C.A., Keating M.T.;
"Elastin point mutations cause an supravalvular aortic stenosis.";
"" Mol. Genet. 0:0-0(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     015337
015337;
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SEQUENCE
                                                                                                                                01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                  InterPro; IPR001179; FKBP_PPIASE.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
PROSITE; PS00453; FKBP_PPIASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                       EMBL; U93037; AAB65620.I; JOINED.
EMBL; U93034; AAB65620.1; JOINED.
EMBL; U93035; AAB65620.1; JOINED.
EMBL; U93036; AAB65620.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998
01-JAN-1998
                                                                                                                     Elastin (Fragment).
                                                                                                                                                                                                                                                                                                            NON
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                                                                                 NCBI_TaxID=9606;
                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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Similarity 100.0%;
L1; Conservative
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                                                                                                                                                                                                                                                                                        602
602 AA;
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                                                                                                              (Human).
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51807 MW;
                                                                                            Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Boak B.B., Atkinson
                                                                                                                                23,
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23,
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Last annotation updat
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Pred.
                                                                                                                                                                                                                                                               Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Ve Catarrhini;
                                                                                            Craniata; Vo
Catarrhini;
                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                         53B5B9A71EF04807 CRC64;
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                                                        Atkinson
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                                      obstructive
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                                                                                                                                                                                                                                                               54;
                                                                                            Vertebrata;
i; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vertebrata; Euteleostomi;
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                                                       D.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                               vascular disease
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                                      vascular
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                                                       Ensing
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                                                                                                     Euteleostomi;
                                                       G.J.,
                                      disease
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RESULT 9
Q1423
ID Q1424
AC Q143
AC Q14
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Q8NBI4
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Best Local S
Matches 11
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Best Local Similarity
Matches 11; Conserv
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EMBL; U93036; AAB65621.1; JOINED.
InterPro; IPRO01179; FKBP PPIAse.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
PROSITE; PS00453; FKBP PPIASE_1; 1.
NON_TER 1 1
NON_TER 635 635
SEQUENCE 635 AA; 55279 MW; 729500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saito K., Yamamoto J., Wakam Nagahari K., Sugano S., Isog "HRI human cDNA sequencing p Submitted (MAR-2002) to the EMBL; AK07554 "BAC11696.1;
                                                                                                                                                                                                                                                                                     Q14235;
Q14235;
Q1-NOV-1996
Q1-DEC-2001
Q1-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8NBI4
Q8NBI4;
01-OCT-2002
01-OCT-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein NTZRP3003474.
Homo sapiens (Human).
Eukaryota; Merarro
NCBI_TaxID=9606;
(11)
SEQUENCE FROM N.A.
MEDLINE=87274906; PubMed=3038460;
                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001179; FKBP_PPIase.
InterPro; IPR000158; FtsZ.
InterPro; IPR000779; tropoelastin.
PRINTS; PR00423; CELLDVISFTSZ.
PRINTS; PR01500; TROPOELASTIN.
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Ota T., Nishikawa T., Suzuki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                          Elastin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. SEQUENCE 643 AA;
                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00453; FKBP_PPIASE_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAAAAAAAAK 276
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K., Sugano S., Isogai T.;
                                                                                                                                                                                                                                                                                         (TrEMBLiel.
(TrEMBLiel.
(TrEMBLiel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Primates;
                                                                                                                               Chordata;
Primates;
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19,
23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    project.";
                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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Pred. No. 56;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45;
Pred. No.
                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FDFC042617E72A69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72950C364127B2A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawai-Hio
                                                                                                                                                                                                                                                                                                                                                                                                                           687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 643;
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Nakamura Y.,
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proc. Natl. Acad. Sc
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MEDLINE=87289668; PubMed=3039501;
Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Rosenbloom J.C., Peltonen L., Rosenbloom J.;
Ralternative splicing of human elastin mRNA indicated analysis of cloned genomic and complementary DNA.";
Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
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"Structure of the
of Alu repetitive
                                                                                                                                                                                                                                                                                    MEDLINE=87274906; PubMed=3038460;
Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
Rosenbloom J., Ornstein-Goldstein N.;
"Structure of the 3' region of the human elastin gene: great
of Alu repetitive sequences and few coding sequences.";
Connect. Tissue Res. 16:197-211(1987).
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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Ffeiffer B.D.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Lii J., Li Z., Liang Y., Lin X.,
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EMBL; M16983 AAC98395.1; JC
EMBL; M17265; AAC98395.1; JC
EMBL; M17266; AAC98395.1; JC
EMBL; M17266; AAC98395.1; JC
EMBL; M17267; AAC98395.1; JC
EMBL; M17270; AAC98395.1; JC
EMBL; M17271; AAC98395.1; JC
EMBL; M17273; AAC98395.1; JC
EMBL; M17274; AAC98395.1; JC
EMBL; M17275; AAC98395.1; JC
EMBL; M17276; AAC98395.1; JC
EMBL; M17276; AAC98395.1; JC
EMBL; M17276; AAC98395.1; JC
EMBL; M17279; AAC98395.1; JC
EMBL; M17270; LEROUNTY; EMBL; M17281; AAC98395.1; JC
EMBL; M17281; AAC98395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9W2V2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit tly)
Eukaryota; Metazoa; Arthropoda; Haxapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CG32683 protein.
CG32683 OR CG288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
PROSITE; PS00453; FKBP_PPIASE 1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neoptera; Endopterygota;
Ephydroidea; Drosophilid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAAAAAAAAAK 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CG2881 OR CG2883 OR melanogaster (Fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diptera; Brachycera; Muscomorpha; ae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOINED
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Last sequence update)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CG15303.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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RESULT 12
Q23590
ID Q2359
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy L., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Melson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Sunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
"The genome sequence of Drosophila melanogaster.";

RA ROSCENCE 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CeIniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

VA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Ranzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

VA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

VA Dodson K., Dorsett V., Doup L.E., Doyle C., Dreenek D., Farfan D.,

Rerriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

VA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

VA McIntosh T.C., Moy M., Kruse D., Li P., Mattei B., Moshrefi A.,

VA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

VA Pacleb J., Paragas V., Park S., Patel S., Pfeifer B.,

VA Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

VA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

VA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

"Sequencing of Drosophila melanogaster genome.";

"Staphmitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                         Matches
                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
"Annotation of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                             FlyBase; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003450; AAF46586.2; -
HSSP; P08168; 1CF1.
FlyBase; FBgn0052683; CG32683.
InterPro; IPR000698; Arrestin.
  Q23590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2000)
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[3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Adams M.D., Celniker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                PF00339; arrestin; 1.
PF02752; arrestin_C; 1.
pm; PD002099; Arrestin; 2.
                                                                                                685
                                                                                                                                                                     11;
                                                                                                                                   1 AAAAAAAAAAK 11
                                                                                                                                                                                           Similarity
                                                                                              AAAAAAAAAAK 695
                                                                                                                                                                                                                                                    804 AA;
                                                                                                                                                                         Conservative
  PRELIMINARY;
                                                                                                                                                                                                                                                    87536 MW;
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                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gibbs R.A., Rubin G.M., Vente
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                       0;
                                                                                                                                                                                           Score 45;
Pred. No.
  PRT;
                                                                                                                                                                                                                                                    06244F0D8A9CB635 CRC64;
                                                                                                                                                                       Mismatches
  1430 AA.
                                                                                                                                                                                                              DB 5;
                                                                                                                                                                       0;
                                                                                                                                                                                                              Length 804;
                                                                                                                                                                         Indels
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RESULT 13
Q8XTG0
ID Q8XTG
AC Q8XTG
DT 01-MJ
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Best Local
                                                                                                                                                                   Matches
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SMART; SM00297; BROMO; 1.
SMART; SM00571; DDT; 1.
SMART; SM00391; MBD; 1.
SMART; SM00391; PHD; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Couper J., Coulson J.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
"elegans.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-1994
[3]
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Q8XTG0;
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                Pfam; PF00439; bromodomain; 1.
Pfam; PF02791; DDT; 1.
Pfam; PF01429; MBD; 1.
Pfam; PF00628; PHD; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Favello A., Vaudin M.;
"The sequence of C. elegans
Submitted (NOV-1994) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECTENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZK783.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZK783.4 protein.
                                         Q8XTG0
                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001487; Bromodomain.
InterPro; IPR004022; DDT dom.
InterPro; IPR001739; Methyl-CpG bind.
InterPro; IPR001965; Znf_PHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U13646; AACZY
HSSP; Q92831; 1B91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              wormPep; ZK783.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lature 368:32-38(1994).
                                                                                                            114
                                                                                                                                     щ
                                                                                                                                                                              Similarity
                                                                                                                                                                                                                               PS50014; BROMODOMAIN_2; 1.
PS50016; ZF_PHD_2; 1.
                                                                                                                                     AAAAAAAAAAK 11
                                                                                                            AAAAAAAAAAK 124
                                                                                                                                                                                                                      1430 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JUN-1998)
                                                                                                                                                                   Conservative
                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACZ4421.1;
                                                                                                                                                                                                                                                                                                                     BROMODOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              CE18461.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                100.0%; Score 45; DB 5;
100.0%; Pred. No. 1.1e+02;
live 0; Mismatches 0;
                                                                                                                                                                                                                     PHD 2; 1.
160457 MW;
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08,
23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cosmid ZK783.";
EMBL/GenBank/DDBJ
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                                          PRT;
                                                                                                                                                                                                                      70749892B6859D70 CRC64;
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                                                                                                                                                                                          Length 1430;
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Bacteria; Proteobacteria; Plasmid megaplasmid.

Betaproteobacteria; Burkholderiales;

Ralstonia solanacearum (Pseudomonas

RSP0151 OR RS02969

Putative

RHS-related protein.

01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

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QBCH17 14
QBCH1 OBCH1
AC QBCH1
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Q8VH35
            S E E
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Best Local Similarity
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Best Local
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Q8VH35 PRELIMINARY; PRT;
Q8VH35;
01-MAR-2002 (TrEMBLrel. 20, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Sprague-Dawley; TISSUE-Mammary gland; Shan L., Yu M., Snyderwine E.G.; "Cloning and functional nanlysis of rat Id4 gene."; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AF468681; AA015695.1; -. SEQUENCE 161 AA; 16621 MW; 2AB9EZD69C3909ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR005074; Peptidase C39.
InterPro; IPR006530; YD.
Pfam; PF03412; Peptidase C39; 1.
TIGRFAMs; TIGR01643; YD_repeat_2x; 14.
Plasmid; Complete proteome.
SEQUENCE 1710 AA; 187661 MW; AACD8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helix-loop-helix protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.3%;
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Last sequence update)
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Pred. No. 44;
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Pred. No. 1.3e+02;
; Mismatches 0;
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                                                                                          276 AA
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Best Local :
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                                                                                              Pfam; PF00505; HMG box; 1.
PRINTS; PR00308; ANTIFREEZEI.
SMART; SM00398; HMG; 1.
                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                           SOX21.
                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                    SEQUENCE
                                                                                                                                                                        Uwanogho D.A.;
                                                                                                                                                                                 STRAIN-BALB/cJ;
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                     HMG-box protein.
                                                                                                                                                                                                                NCBI_TaxID=10090;
137
                                         10;
                    1 AAAAAAAAAAK 11
                                                    Similarity
AAAAAAAAAR 147
                                                                                    276 AA;
                                         Conservative
                                                                                                                                                                                                                            Chordata;
Rodentia;
                                                                                    28593 MW;
                                                   93.3%;
                                                                                                                                                                                                                                                                               20,
                                                                                                                                                                                                                                                                               Last sequence update)
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                                         1;
                                                             Score 42;
                                                    Pred.
                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                    24A31E0FE24A9078 CRC64;
                                          Mismatches
                                                    No.
                                                     70;
                                                             DB 11; Length 276;
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Search completed: February 19, Job time : 37 secs 2004, 10:04:30